Applicants: Ron S. Israeli, et al. U.S. Serial No. 08/466,381 Filed: June 6, 1995

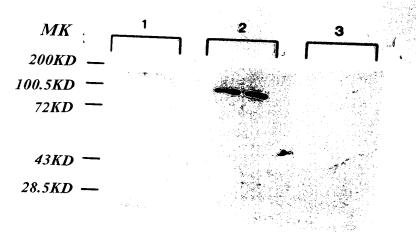
BEST





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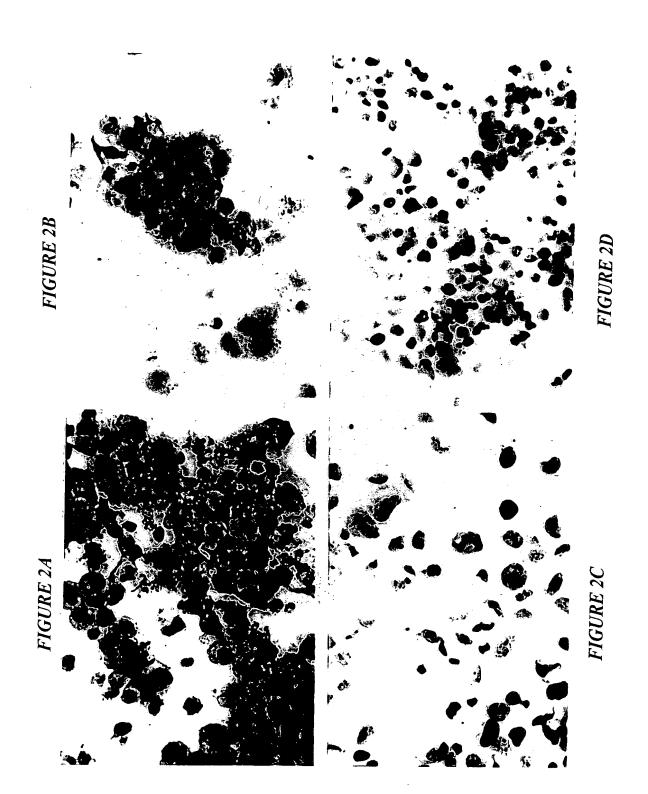
FIGURE 1

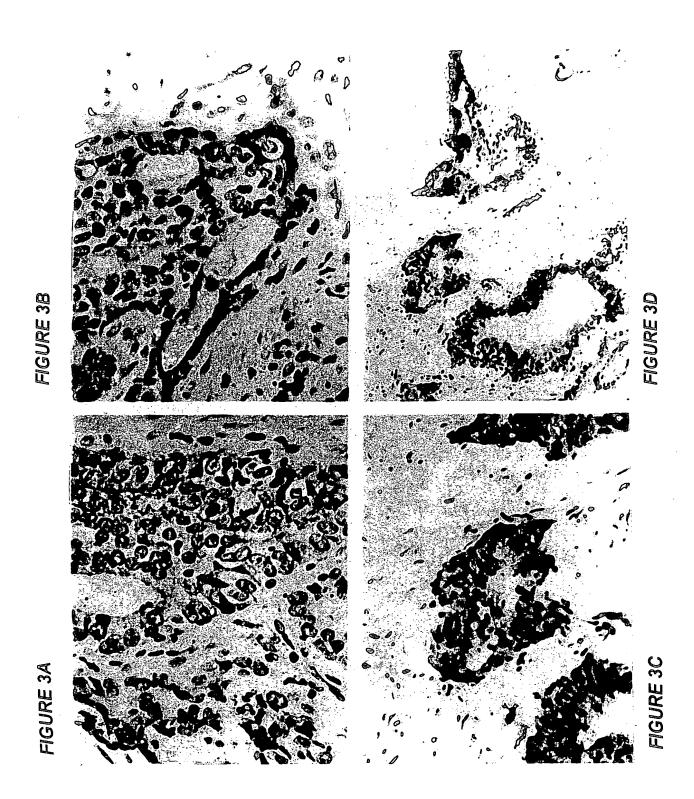


1 - anti- EGFr PoAB RK-2

2 - Cyt-356 MoAB/RAM 3 - RAM

2/48 BEST AVAILABLE COPY

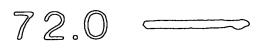




4/48

FIGURE 4

100.5

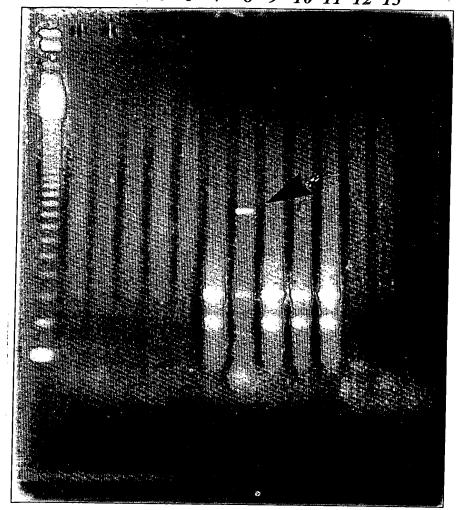


43.0

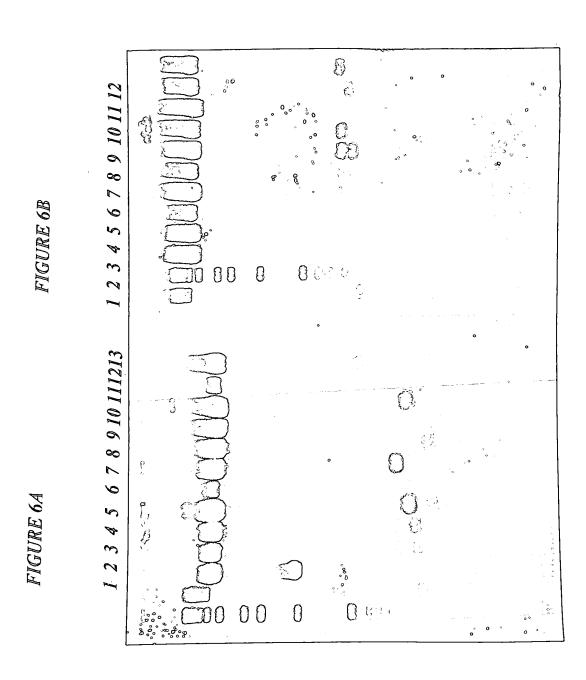
28.5

5/48

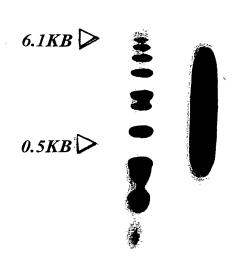




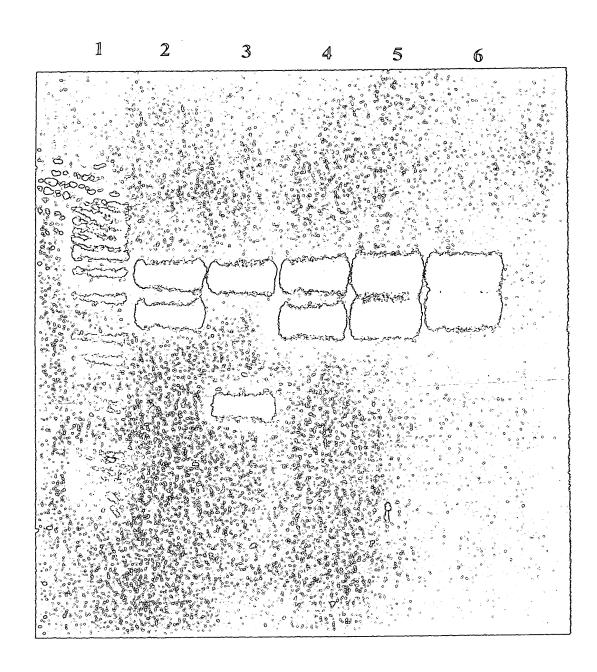
6/48



7/48



8/48



9/48

FIGURE 9

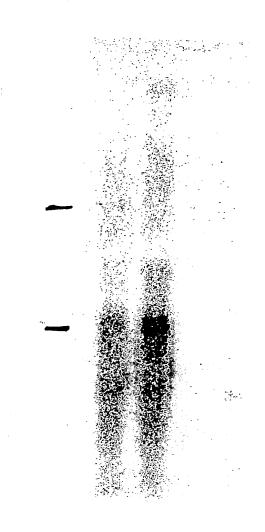
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FIGURE 11

9.5 7.5

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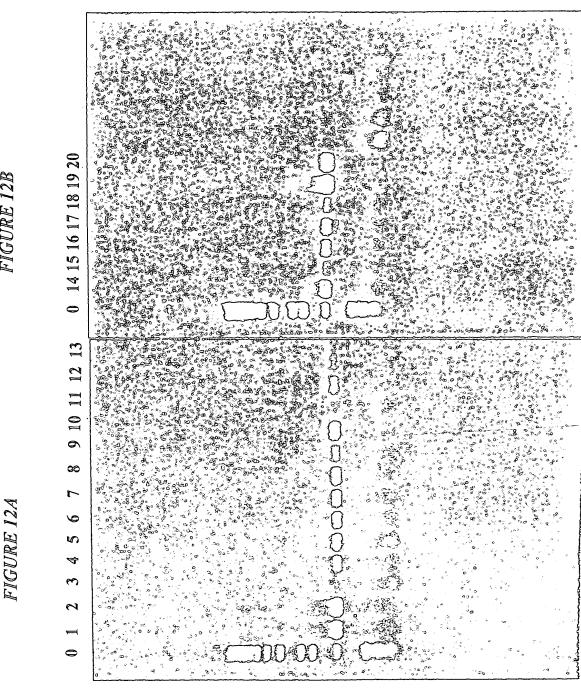
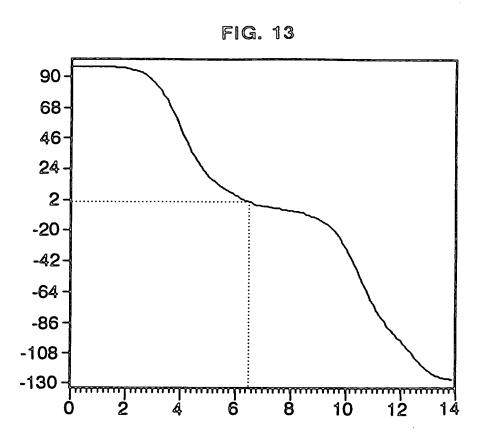


FIGURE 12B



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sequence.

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Analysis

750°

residues is:

PMSANTIGEN.

on sequence

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Total number of

FIG. 14-1

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shown with conformation codes Sequence

о П given conformation ๙ i D residues More ប្ដ മ Ç O Consecutive stretch overlined

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FIG. 144

Semi-graphical output.

semi-graphical representation: Symbols used in the

conformation: conformation: Extended Coil \bowtie conformation: conformation: Helical Turn

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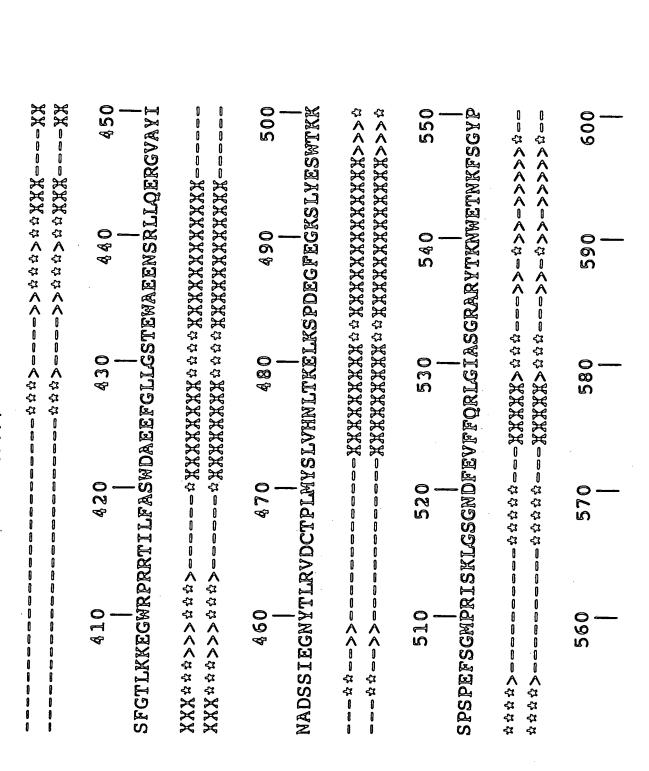
100 nitpkhnmkafldelkaenikkflynftqiphlagteqnfqlakqiqsqw ტ ტ (C) (S) 00

FIG. 14.

150	Ddddda:	^	200	- INCSGKI
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0 –	hpnyisine	# 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	087	lvyvnyarte
120	OVLLSYPNKT	{}	170	- Spocmpecd
011	KEFGLDSVELAHYI	**************************************	160	YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI
	120 130 140	120 	110 120 130 140 150 150 150 150 150	110 120 130 140 150 150 150

	250 NLPG	^ ^ ;; ;; ;; ;; ; ;	300 	0 0 0 0 0 0	350 	1 4 4 4 4 4 4 4	400	IVR
**************************************	240 YFAPGVKSYPDGWI	<	290 Eavglpsipvhp		310 320 330 340 350 KMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKWHIHSTN	;;XXXXXX;;	900	 GIDPQSGAAVVHE
	230 VILYSDPAD	0 D 0 O	280 NEYAYRRGIA	:===XX====:	330 VPYNVGPGFT	0 0 0 0 0 0 0 0 0 0 0 0	380 380	 GGHRDSWVFG
>	220 knaqlagarg	XXXXXXXX¤¤<<	270 GDPLTPGYPA	фесееефффее фесее	320 PDSSWRGSLK	->>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	370	AVEPDRYVIL
	210 220 230 240 250 VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG	\$\$<<0000000000000000000000000000000000	260 270 280 290 300 CGVQRGNILNLNGAGDPLTPGYPANEYAYRGIAEAVGLPSIPVHPIGYY	0 \$\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	310 Daqkllekmggsap	XXXXXXX=>>>>\$\$\$\$XXXXX	360	EVTRIYNVIĞTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR

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Lyhsvyetyekfydpmfkyhltvaqvrggmvfelansivlpfdcrdy	ekfydpmfkyhi	Ltvaqvrggw	VFELANSIVLP	FDCRDY
KXXXXX	-X-XXXXXXXXXXXXXXXX-X-	X-X	XXXXX	XXX<
610 620 630 640 650 AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERL	620 - SISMKHPQEMK	630 TYSVSFDSLF	640 Savknfteias	650
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	HWNDQLMCLER	AFIDPLGLPD	 RPFYRHVIYAP	SSHNKY
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710 720 730 740 750 AGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA	720 FDIESKVDPSK	730 Bangevkrqiy	740 Vaaftvqaaae	750 TLSEVA
{XXX<	->-XXXXXXX\$\$\$\$XXXXXXXXX<-	0 0 0 0	XXXXXXXXXXXXXXXXXXXX	XXXXXX

FIG. 15A

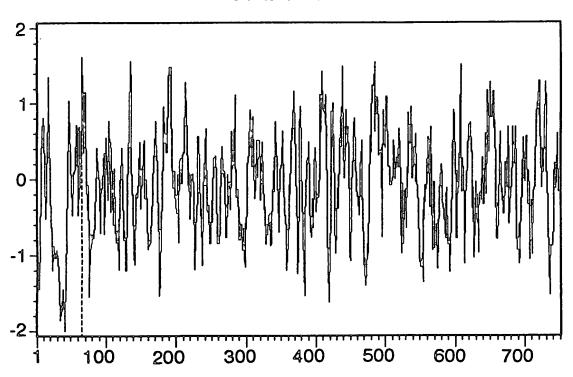


FIG. 15B

Done on saquence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence

authors The averaging group length is: 6 amino acids. The method used is that of Hopp and Woods. by the the value recommended .≃ -> This

2 K highest points of hydrophilicity three The

Asp-Glu-Lau-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu ලා ලා 137 r O 132 ന ശ From From From 1.62 1.57

Lys-Ser-Pro-Asp-Glu-Gly & @ **7** 800 From

Ah stands for: Average hydrophilicity.

the highest point was in 100% The second and third points dronb. of incorrect predictions omiy a known antigenic control proteins, Note that, on a group of of the cases assigned to proportion of 33% ଟ ga∨@

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nitn 203	1 6 4 6 5	203	10 CACA	 	11: rctt :: Actao	1190 AAAATGGG' :::::::
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• .	ه د		060 ACC	ACCC 10	120 CTGT :: CTTC	1180 CTAGA
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FIG. 16-1

CTGG AA 1210	aagt aaga	ATGT Seese	AAGC AAAC
1250 TTGGAC : ::: TGAC	1310 CCAATGAAG ::: ::: CCATGAAAG	1370 ACAGATI : ; ; ATCGGTI	1430 CTCAGAGTGGAC :: :::: CTGGCACTGGAA
12 CAATGTT :: :: TAAGGT-	131 CTACCA : ::: NTTCCA	13 PAGAC :: TGAT	1430 :TCAGAG : :TGGCAC
40 CTACAL :: :: CTGTAL	00 CCACTC :: GAACAA 250	360 TGGAACC :::::: AAGAACC	SACCC SACCC SAAGC
1240 GCCCTA ::: TTCCTG	1300 CATCCA : : TGTGAA 1250	1360 AGTGG : : TGAAG	1420 TATTGA ; ; 3GCTAA 1370
AAAGI :	ATGCA(;;;TAGA;	GAGC	GTGG' ; ; Gagt
1230 GTCTC2 :: CGATC(80 1290 CAAAAGTCAAGATGC ::::::::::::::::::::::::::::::::::::	1350 CAGAG : : : CCAGG	1410 GTTTGGTG ;;; CCCAGGAG
GGAAG :: GGTGC	laage :: Tege	CTCTC	GGGTC ::::
1200 1210 1220 1230 1240 1250 AGCACCACCAGATAGCTGGAGGAAGTCTCAAAGTGCCTACATGTTGGACCTGG ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	70 1280 1290 1300 1310 CTTTTCTACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT : : : : : : : : : : : : : : : : : : :	1320 1330 1340 1350 1360 1370 GACAAGAATTTACAATGTGATACTCTCAGAGGAGCAGTGGAACCAGACAGA	1380 1490 1400 1410 1420 1430 CATTCTGGGAGTCACGGACTCATTGGTGGTATTGACCCTCAGAGTGGAGC i i i i i i i i i i i i i i i i i i i
AGCTC	rctac : :	TGATZ	14 GGGAC GAGAC
1210 Gatage Ga-ag-	70 CTTT1	30 CAATG	CACCCCACCCCACCCCACCCCACACACACACACACACA
12 ACCAGA : :: CTCTGA	1270 TGGAAACT ::: AGGAGA	1330 TTTACAA :: TTCTGAA 1280	1390 GGAGGTC ::::: GGAGCCC
0 ACCA(: ATGCY	D FACTGGA F F F F F F F F F F F F F F F F F F F	AGAA' * * * * * * * * * * * * * * * * * * *	CTGGG
	1260 12 CTTTACTGGAAA ; ;;; ; CAAAGCAGGAGA	1320 13 GACAAGAATTTA ; ; ; ; CAGGAAGATTCT	1380 CATTC : : 1330
pmsgen CHKTFE	1260 1270 1280 1290 1300 1310 pmsgen CTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT i i i i i i i i i i i i i i i i i i i	pmsgen CHKTFE	pmsgen (CHKTFE 1
D E	pm CH]	pms	pms

1490 AAGGGTGGAG : : : : AGGGCTACAA 1440	1550 TTCTTGGTTC : : : : : : : : : : : : : : : : : : :	1610 CTTATATTAA :::::::: CTTACATCA-	1670 ACCGCTGATG :: :: :: CCCCTTGCTG
1480 ACTGAAAAAGGAA	1540 GARTTTGGTC ::: :: GACTACGGAG 1490	1600 ;cGTGGCGTGG ; ; ; ; ; ; ; ;	1660 STTGATTGTAC :: ATTTCTGCCAG
1440 1450 1460 1470 1480 1490 AGCTGTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGTGGAG ::::::::::::::::::::::	1500 1510 1520 1530 1540 1550 ACCTAGAAGAACTTTGTTTTGCAAGCTGGGATGCAGAATTTTGGTCTTTTTTTT	1560 1570 1580 1590 1600 1610 pmsgen TACTGAGTGGCAGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAA iiiiiiiiiiiiiiiiiiiiiiiiiiiii	1620 1630 1640 1650 1660 1670 TGC-TGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG :: :: :: :: :: :: :: :: :: :: :: :: ::
1460 rgtgagga : ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	1520 STTTGCAAGCT X:::: :::: X::::	1570 1580 GAGGAGATTCAAGAC :::::::::: GAGGGTACTCTGCCA	1640 AAGGAAACTA- ::::::::
1450 TTCATGAAATTG : ::: ::: TGTTGGAACTTG 1400	1510 GAACAATTTT ::::: GAAGCATCAT	1570 TGGGCAGAGGA(::: ::: TGGCTGGAGGG(1630 TCATCTATAGA : :: : TGCTCCAGTC
		1560 TACTGAGT ::::::: TACTGAAT	
pmsgen CHKTFE	pmsgen	pmsgen CHKTFE	pmsgen CHKTFE

1730 GAAGGC :: :: GAGAGC 580	1790 ATGCCC	CTGGA
1730 1730 1730 1730 1730 1730 1730 ACCTAACAAAGCTGAAAAGCCCTGATGAAGGCTTTTGAAGGC i i i i i i i i i i i i i i i i i i i	1750 1760 1770 1780 1790 BAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC	GTTCCTCTTGGC 1730
1710 ;::::::::::::::::::::::::::::::::::::	1770 GTCCTTCCCCAG	GTAAAAGCAGTI 1720
1700 FAACAAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1760 CTAAAAAAA	CCAGACTGG 1710
1690 ACAACCTAA ; ; ; GGAGTATTA	1750 1760 AAAGTTGGACTAAAAA	&GACTTGGC 1700
1680 1690 1700 1710 1720 1730 1730 1730 1730 1730 1730 1730 173	Dmsgen AAATCTCTTTATG	CICTATAACAGACTTGGCCCAGACTGGTAAAGCAGTTGTTCCTCTTGGCCTGGA 1710 1720 1730
pmsgen CHKTFE	pmsgen	

RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAAATGTGAAGCTCACTGTGAACAATGTACT AGTIGGAATATAGATIC pmsgen ccaccagaraccagaragagagagrorcaaagroccracaargrogaccrg 164 pmsgen -TACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATC-CACTCT-ACCAATG 164 00 1250 1300 RATTRF TGCAGAAAAGCTATTCAAAAACATGGAAGGAAACTGTCCTCCT end. 1240 Rat transferrin receptor mRNA, 1290 640 1230 identity in 560 nt overlap 1280 000 069 1220 1270 00 680 1210 1260 55.5% RATTRFR

FIG. 16-5

1370 CAGACAG ::::::	1430 CTCAGAG ::::	1480 AAAAGGAA ::::::	40 TGGTCTT ::::
1360 AGTGGAACCAGACA : :::::::::: IGAGGAACCAGACC	1420 FATTGACC : :: TTGCGAAG 840	14 ::: NTGATTTC	1530 1540 TGCAGAAGAATTTG
1320 1330 1340 1350 1360 1370 pmsgenAAGTGACAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAG iii iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	1390 1400 1410 1420 1430 GGAGGTCATGGTGTTTGGTGTATTGACCCTCAGAG ::::::::::::::::::::::::::::::::::	1440 1450 1460 1470 1480 pmsgen T-GGAGCTGTTGTTCATGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA ;;;;;;;;;;;;;;;;;;;;;;;;;;	- a 5 -
13 TACTCTCA ; ; ; CGTTATTA	141 ATGGGTGTT :::: TTGGGGCCC	OGGAGCTTT	1510 ATTTTGTTTGCAAGCTGGGA ::::::::::::::::::::::::::::::::::
1340 TGTGATAGGT ; ; ; CATCTTTGGC	1400 CGGACTCATGGG : ::: : :::: AGAGACGCTTGGG	1460 AATTGTGAG	1510 ATTTTGTTT ::: :::: ATTATCTTT(
1330 TTACAATC :: ACTTAACI	1390 GGAGGTCACC :::: :: GGAGCCCAGA	1450 TTCATGAAATT : :::::: CTGTTGAAACT 870	O 15 AAGAACAAT ;;;;;; CAGGAGTAT
1320 Gacaagaat ::::::::	1380 CATTCTGGG : : : : : TGTAGTAGG	1440 AGCTGTTG :: : :: AGGTCTT	1500 AGACCTAGA X:::::::
1: AAGTG	Tatgi : : : Tacat	1440 pmsgen T-GGAGCAGCTGT ; ;;; ;;; ;; RATTRF TGGGAACAGGTCT	1490 GGGTGGAC :: : X: GGATTTAC
pmsgen - RATTRF G	pmsgen A' RATTRF C'	pmsgen RATTRF	pmsgen RATTRF

	1730	1740		1750	1760	1770
pmsgen	pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAAGTCCTTCCCCAG	CAAATCTCTT	Tat-gar	AGTTGGAC	CTAAAAAAGT	rcctrcccag
	000000000000000000000000000000000000000	00	000000000000000000000000000000000000000	00		8.0
RATTRF		AAAATATCTA	TATCGAAACA	GTAATTGGAT	PTAGCAAAATT	TTGATGGAAAATATCTATATCGAAACAGTAATTGGATTAGCAAAATTGAGGAACTTT
	1140	1150	1160	1170	1180	1190
	1780	1790	1800	1810	1820	1830
pmsgen	pmsgen AGTTCAGTGCCATGCATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT	CATGCCCAGG	ATAAGCAAAT	TGGGATCTGG	FAAATGATTT	IGAGGTGTTCT
RATTRF	CCTTGGACAATGCTGCATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC	rgctgcattc	CCTTTTCTTG	CATATTCAGG	BAATCCCAGCE	Հ Դորու Հորորդում
	1200	1210	1220	1230	1230 1240 1250	1250

1460 1470 1480 1490 1500 pmsgen AAATTGTGAGGACTTTGGAACACTGAAAAAGGAAGGTGGAGACCTAGAACAA iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	1510 1520 1530 1540 1550 1560 TTTTGTTTGCAAGGATGCAATTTGGTCTTCTTGGTTCTACTGGCAGGCA	1570 1580 1590 1600 1610 1620 A-GGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTTATTAATGCTGACTCATCT :::::::::::::::::::::::::::::::	1630 1640 1650 1660 1670 1680 ATAGAAGGAAACTACACTCTGAGATTGTACACCGCTGATGTACA-GCTTGGT-AC
480 1490 AAAAGGAAGGGTGGAGA ::: X::: TAAAAGATGGGTTTCAG	1550 TCTTCTTGGTTCT :::::::	1610 TGCCTTATATTAAT : :::::::X CACTTATATTAAT	1670 CACCGCTGATGTA ::::::::::::::::::::::::::::::::
1480 ACACTGAAAAA 	1530 1540 TGCAGAAGAATTTGG :::::::::::::::::::::::::::	1600 GAGCGTGGCGT ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	GTTGATTGTAC
1470 SGAGCTTTGGA. : : : CGTTCTCAGATA	CTGGGATGCAC ::: ::: ; TTGGAGTGCTC	O 1590 GACTCCTTCAA(; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	0 1650 ACACTCTGAGA(;; SSSACTTCAAGO)
1460 pmsgen AAATTGTGAG :::::::::::::::::::::::::::::::::::	1520 TGTTTGCAAG : ::::::::::::::::::::::::::::::::::	70 158 GGAGAATTCAAG	GAAGGAAACTA
pmsgen AAA :: HUMTFR AAC 1380	1510 pmsgen TTT :: HUMTFR TTA	1570 pmsgen A-GG : :: HUMTFR AGGG	1630 pmsgen ATAG : HUMTFR GTTC

FIG. 16-10

	⊃ 0 0 =		0	O 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	⊃₹ / ₹	0 %/₹
pmsgen	ACAACCTAACAA	aacaaaaggc	TGAAAAGCCCT	IGATGAAGGC	ITTGAAGGCA	AAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATG
	00	00				
HUMTER	AAAACAATGCAAAA	TGCAAAATGTG	AAGCATCCGG1	TRACTGGGCA.	ATTTCTATA	ATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC
	1620	1630	7640	1650	1660	1670

FIG. 16-11

35/48

FIGURE 17A

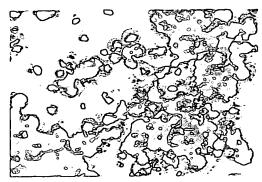


FIGURE 178

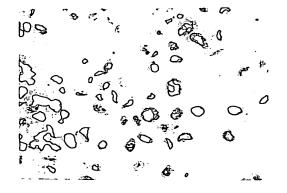


FIGURE 17C

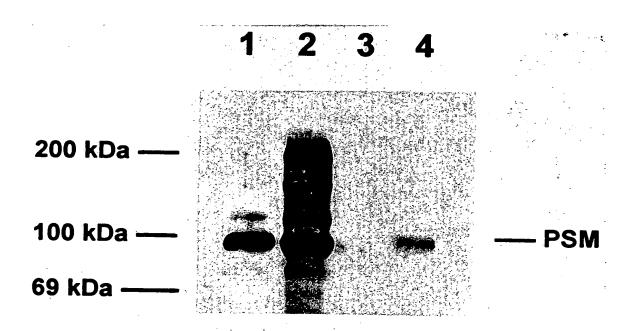


36/48

FIGURE 18

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37/48

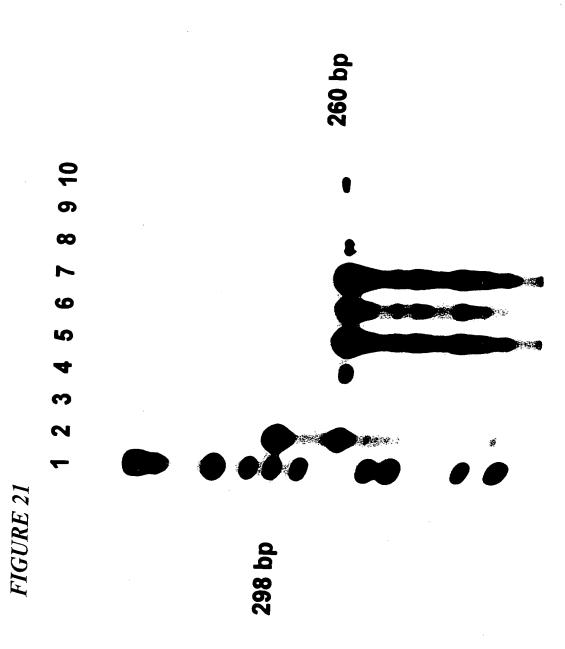


38/48

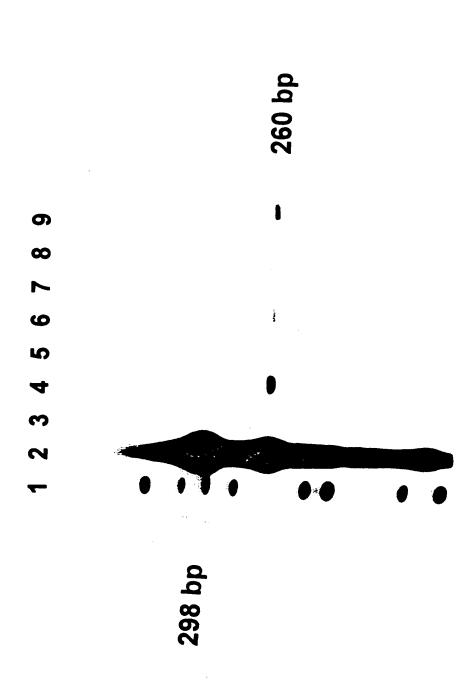
10 <u>6</u> 89 12 $^{\sim}$ **√** 10 **® @** 2 ම ശ \$ જ \otimes \triangle

FIGHTRE 2

39/48



40/48



41/48

				
CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	
A9(11) (A9+HUM. 11)	YES	NO	_	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	_	_
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	_	-
R1564 (RAT MAMMARY)	NO	YES	-	_
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES		REPEAT
R1564-11-c16	YES	YES	_ ,	ND
R1564-11-c12	YES	YES	ND	+

42/48



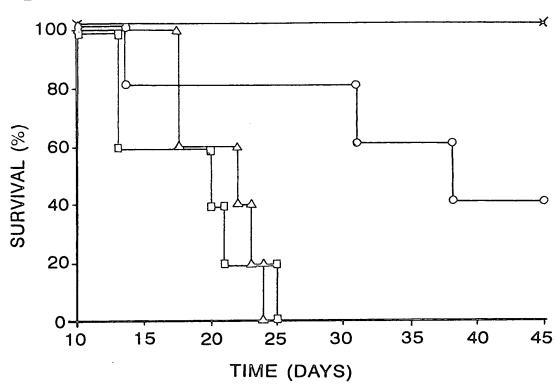
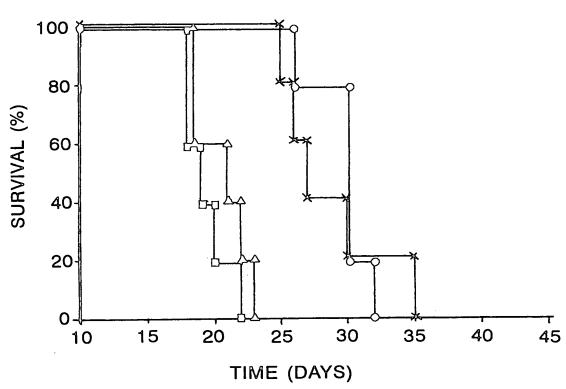
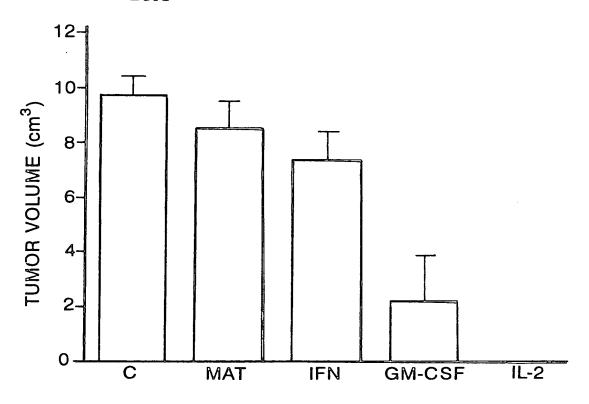


FIGURE 24B

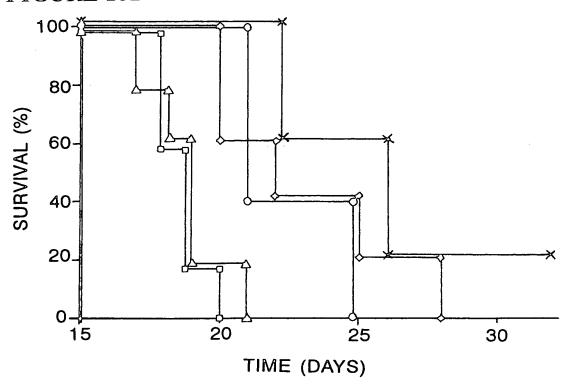


43/48

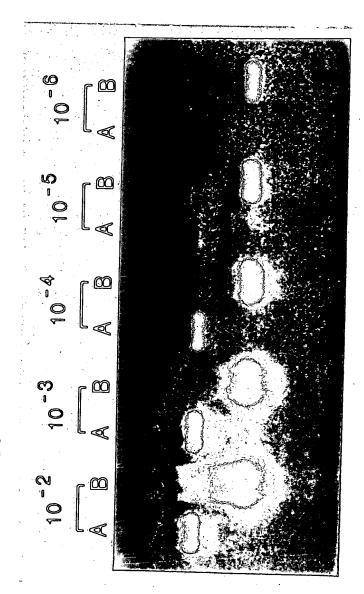
FIGURE 25A



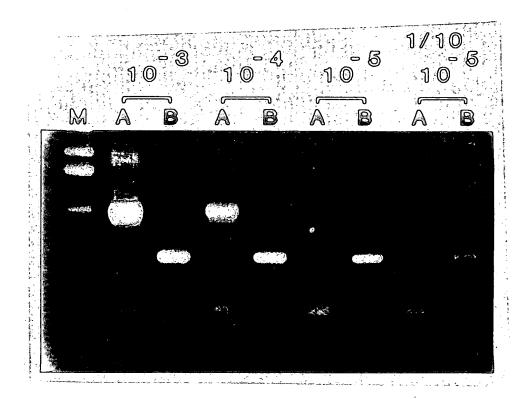




44/48



45/48



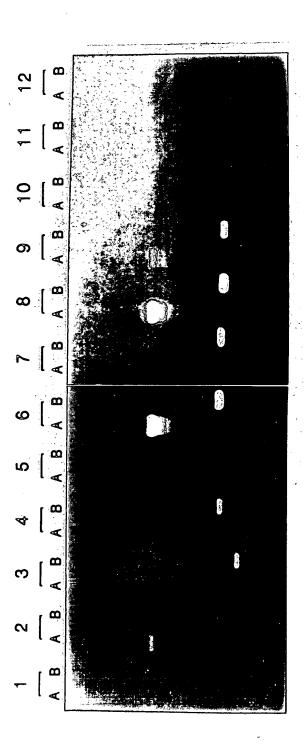


FIGURE 28

47/48

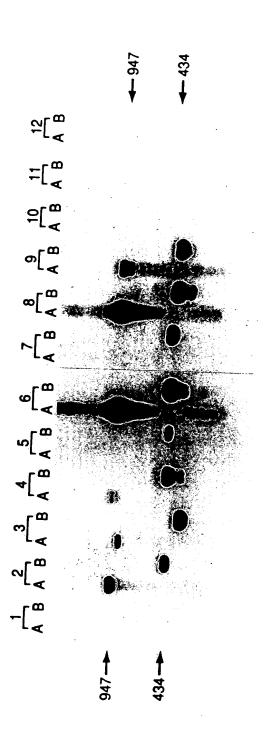


FIGURE 29

48/48

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	_	+
2	T2NoMo	RRP 7/93	6.1	_	_	+
3	T2CNoMo	PLND 5/93	4.5	0.1	_	+
4	T2BNoMo	RRP 3/92	NMA	0.4	_	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	_	+
6	Recur T3	I-125 1986	54.7	1.4	_	+
7	T3ANoMo	RRP 10/92	NMA	0.3	_	+
8	T3NxMo	XRT 1987	7.5	0.1	_	_
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5		+
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	_
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	_	_
16	T2CNoMo	RRP 4/92	0.1	0.3	-	_

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